



SEQUENCE LISTING

<110> MERKULOV, Gennady V. et al

<120> ISOLATED HUMAN TRANSPORTER PROTEINS,
NUCLEIC ACID MOLECULES ENCODING HUMAN TRANSPORTER PROTEINS,
AND USES THEREOF

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<140> 09/768,781

<141> 2001-01-25

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<170> FastSEQ for Windows Version 4.0

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<212> DNA

<213> Homo sapien

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			20					25					30		
Thr	Tyr	Arg	Met	Thr	Tyr	Thr	Phe	Ser	Phe	Phe	Met	Phe	Ser	Ser	Ile
		35					40					45			
Met	Val	Gln	Leu	Thr	Leu	Ile	Phe	Val	His	Arg	Asp	Leu	Phe	Pro	Ser
	50					55					60				
Ser	Phe	Leu	Glu	Ala	Ala	Leu	Tyr	Tyr	Arg	Thr	Phe	Val	Gln	Thr	Leu
65					70					75					80
Phe	Val	His	Arg	Asp	Leu	Ser	Phe	Pro	Ala	Ser	Val	Ile	Ala	Ser	Val
				85					90					95	
Phe	Leu	Phe	Val	Ala	Glu	Thr	Ala	Ala	Ala	Leu	Tyr	Leu	Ser	Ser	Thr
			100					105					110		
Tyr	Arg	Ser	Ala	Gly	Asp	Arg	Met	Trp	Gln	Val	Leu	Thr	Leu	Leu	Phe
		115					120					125			
Ser	Leu	Met	Pro	Cys	Ala	Leu	Val	Gln	Phe	Thr	Leu	Leu	Phe	Val	His
	130					135					140				
Arg	Asp	Leu	Gln	Ala	Lys	Asp	Lys	Pro	Leu	Ser	Leu	Phe	Met	His	Leu
145					150					155					160
Ile	Leu	Leu	Gly	Pro	Val	Ile	Arg	Cys	Leu	Glu	Ala	Met	Ile	Lys	Tyr
			165						170					175	
Leu	Thr	Leu	Trp	Lys	Lys	Glu	Glu	Gln	Glu	Glu	Pro	Tyr	Val	Ser	Leu
		180						185					190		
Thr	Arg	Lys	Lys	Met	Leu	Ile	Asp	Gly	Glu	Glu	Val	Leu	Ile	Glu	Asp
		195					200					205			
Pro	Leu	Leu	Met	His	Leu	Leu	Gly	Pro	Arg	Cys	Glu	Tyr	Glu	Glu	Pro
	210					215					220				
Tyr	Val	Ser	Thr	Lys	Asp	Gly	Glu	Ser	Ser	Arg	Asp	Arg	Pro	Leu	Ala
225					230					235					240
Leu	Leu	Met	His	Leu	Leu	Gln	Leu	Gly	Pro	Leu	Tyr	Arg	Cys	Cys	Glu
			245						250					255	
Val	Phe	Cys	Ile	Tyr	Cys	Gln	Ser	Asp	Gln	Asn	Glu	Glu	Pro	Tyr	Val
			260					265					270		
Ser	Ile	Thr	Lys	Lys	Arg	Gln	Met	Pro	Lys	Asp	Gly	Leu	Ser	Glu	Glu
		275					280					285			
Val	Glu	Gln	Trp	Glu	Val	Gly	His	Ser	Ile	Arg	Thr	Leu	Ala	Met	His
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Arg	Asn	Ala	Tyr	Lys	Arg	Met	Ser	Gln	Ile	Gln	Ala	Phe	Leu	Gly	Ser

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Val	Pro	Gln	Leu	Thr	Tyr	Gln	Leu	Tyr	Val	Ser	Leu	Ile	Ser	Ala	Glu
				325					330					335	
Val	Pro	Leu	Gly	Arg	Val	Val	Leu	Met	Val	Phe	Ser	Leu	Val	Ser	Glu
			340					345					350		
Val	Gly	Leu	His	Arg	Ala	Arg	Ser	Ile	Gln	Ala	Phe	Leu	Gly	Ser	Pro
		355					360					365			
Gln	Leu	Thr	Gln	Leu	Tyr	Gly	Arg	Met	Ser	Leu	Ser	Ser	Lys	Glu	Val
	370					375					380				
Gly	Gln	Ala	Glu	Gly	Lys	Leu	Ile	Thr	His	Arg	Ser	Ala	Phe	Ser	Arg
385					390					395					400
Ala	Ser	Val	Ile	Gln	Ala	Phe	Leu	Gly	Ser	Ala	Pro	Gln	Leu	Thr	Leu
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Gln	Leu	Tyr	Ile	Thr	Val	Leu	Glu	Gln	Asn	Ile	Thr	Thr	Gly	Arg	Cys
		420						425					430		
Phe	Ile	Met	Thr	Leu	Ser	Leu	Leu	Ser	Gln	Val	Thr	Tyr	Gly	Ala	Thr
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Leu	Cys	Asn	Met	Leu	Ala	Ile	Gln	Ile	Lys	Tyr	Asp	Asp	Tyr	Lys	Ile
	450					455					460				
Arg	Leu	Gly	Pro	Leu	Glu	Val	Leu	Cys	Ile	Thr	Ile	Trp	Arg	Thr	Leu
465					470					475					480
Glu	Ile	Thr	Ser	Arg	Leu	Leu	Ile	Leu	Val	Leu	Phe	Ser	Ala	Thr	Leu
			485						490					495	
Lys	Leu	Lys	Ala	Val	Pro	Tyr	Gly	Ala	Cys	Asn	Leu	Ala	Ile	Ile	Lys
		500						505					510		
Tyr	Asp	Tyr	Pro	Leu	Cys	Ile	Trp	Arg	Glu	Ile	Arg	Leu	Val	Leu	Phe
	515						520					525			
Leu	Lys	Val	Ser	Ile	Val	Tyr	Gly	Ala	Leu	Arg	Cys	Asn	Ile	Leu	Ala
	530					535					540				
Ile	Lys	Ile	Lys	Tyr	Asp	Glu	Tyr	Glu	Val	Lys	Val	Lys	Pro	Leu	Ala
545					550					555					560
Tyr	Val	Cys	Ile	Phe	Leu	Trp	Arg	Ser	Phe	Glu	Ile	Ala	Thr	Arg	Val
			565						570					575	
Ile	Val	Leu	Val	Leu	Phe	Thr	Ser	Val	Leu	Lys	Ile	Trp	Val	Val	Ala
		580						585					590		
Gln	Phe	Leu	Val	Leu	Asn	Phe	Leu	Ile	Ile	Leu	Phe	Glu	Pro	Trp	Ile
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	610					615					620				
Phe	Ser	Arg	Val	Gly	Thr	Leu	Val	Val	Leu	Ile	Ser	Val	Thr	Ile	Leu
625					630					635					640
Tyr	Ala	Gly	Ile	Asn	Phe	Ser	Cys	Trp	Ser	Ala	Leu	Gln	Asn	Phe	Pro
			645						650					655	
Trp	Ile	Phe	Trp	Ser	Gly	Pro	Asn	Ile	Glu	Lys	Ser	Arg	Val	Gly	Thr
			660					665					670		
Val	Leu	Thr	Leu	Tyr	Ala	Gly	Ile	Asn	Cys	Trp	Ser	Ala	Gln	Ser	Val
		675					680					685			
Ile	Leu	Val	Asn	Phe	Phe	Ser	Phe	Phe	Leu	Tyr	Pro	Trp	Ile	Val	Phe
	690					695					700				
Trp	Cys	Ser	Gly	Ser	Pro	Phe	Pro	Glu	Asn	Ile	Glu	Lys	Ala	Leu	Ser
705					710					715					720
Arg	Val	Gly	Thr	Thr	Ile	Val	Leu	Cys	Phe	Leu	Thr	Leu	Leu	Tyr	Ala
			725						730					735	
Gly	Ile	Asn	Met	Phe	Cys	Trp	Ser	Ala	Val	Gln	Gln	Leu	Arg	Leu	Ala
		740						745				750			
Asp	Arg	Asp	Leu	Val	Asp	Lys	Gly	Gln	Asn	Trp	Gly	His	Met	Gly	Leu
		755					760					765			

His	Tyr	Ser	Val	Arg	Leu	Val	Glu	Asn	Val	Ile	Met	Val	Leu	Val	Phe
770						775					780				
Lys	Phe	Phe	Gly	Val	Lys	Val	Leu	Leu	Asn	Tyr	Cys	His	Ser	Leu	Ile
785					790					795					800
Ala	Leu	Gln	Leu	Ile	Ile	Ala	Tyr	Leu	Leu	Lys	Gln	Asn	Trp	Tyr	Arg
				805						810					815
Glu	Asn	Leu	Phe	Phe	Cys	Leu	Leu	Gln	Leu	Ile	Tyr	Ser	Leu	Lys	Ile
			820						825					830	
Asp	Asn	Pro	Glu	Leu	Ile	Ser	Lys	Ser	Gln	Asn	Trp	Tyr	Arg	Leu	Leu
			835					840					845		
Ile	Tyr	Tyr	Met	Thr	Arg	Phe	Ile	Glu	Asn	Ser	Val	Leu	Leu	Leu	Leu
	850					855					860				
Trp	Tyr	Phe	Phe	Lys	Thr	Asp	Ile	Tyr	Met	Tyr	Val	Cys	Ala	Pro	Leu
865					870					875					880
Leu	Ile	Leu	Gln	Leu	Leu	Ile	Gly	Tyr	Gln	Leu	Ile	Ser	Ile	Asp	Phe
				885					890					895	
Met	Leu	Leu	Phe	Phe	Gln	Tyr	Leu	His	Pro	Leu	Arg	Ser	Leu	Phe	Thr
			900					905					910		
His	Asn	Val	Val	Asp	Tyr	Leu	His	Cys	Val	Cys	Cys	His	Gln	His	Pro
	915						920					925			
Arg	Thr	Arg	Val	Glu	Asn	Ser	Glu	Pro	Ile	Phe	Met	Leu	Phe	Gln	His
	930					935					940				
Pro	Leu	Phe	Val	Leu	Cys	Cys	Arg	Ser	Glu	Pro	Ser	Cys	Thr	Gly	Ile
945					950					955					960
Leu	Phe	Met	Leu	Val	Phe	Tyr	Gln	Phe	Phe	His	Pro	Cys	Lys	Lys	Leu
				965					970					975	
Phe	Ser	Ser	Ser	Val	Ser	Glu	Ser	Phe	Arg	Ala	Leu	Leu	Arg	Cys	Ala
			980					985					990		
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agattttacaa	gatggatact	atggctctaa	tcaattctct	catttcctcc	cactctcggc	180
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tggtatgtac	ttgtgttcca	aaacaatgaa	cgatgctatt	tgggctgtgt	aaactagaat	300
sggaacaaca	agacgtgatc	accctgtgca	tgaaggccat	agctgcagag	tgtgtaattt	360
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<210> 21
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 <212> DNA
 <213> Homo sapien

<400> 21						
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gacgtgatca	ccctgtgcat	gaaggccata	gctgcagagt	gtgtaatttt	atttaaaaaa	300
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gccgggtgtg	gtgggtcatg	cctgtaatcc	cagcactttg	ggaggctgag	gcggtgggat	540
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a						601

<210> 22
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taatagtatc	aagtatttcc	attcagattg	ccttgaagtg	gaaagaatgc	acttaatcct	180
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gagatgttgc	aaaacttatg	agttcaggag	taaggaatgg	accaagtttg	tcttgattgc	300
ragagaggca	gacaactgca	gtcagccgag	gaatatgggt	cagagtgttg	caatgggaag	360
atacctcatc	attagacaac	taaaaagtct	gtgaaactaa	ttaaggatgg	aactcactcc	420
tttataaaat	ttcatatctg	tacacatgta	taatttttat	ttgtcactta	tacctcaata	480
aggccaaaaa	aattttttat	caataaattt	ttaagtgggg	aggaatcgat	taggctctat	540
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c						601

<210> 23
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tcagagagaa	tatgggat	caatggaaac	agtggcctga	aatttggagt	ctagtcttcc	300
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<210> 24

<211> 601

<212> DNA

<213> Homo sapien

<220>

<221> variation

<222> (301)...(301)

<223> A may be either present or absent

<400> 24

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gcagtggctc	atgcctgtaa	tctcagcact	ttgggaagct	gaggtgggtg	gatcacctga	240
ggtcaggagt	tcaagaccag	cctggccaac	atggtgaaaa	cccgtctcta	ctaaaaatac	300
aaaaaaaaaa	aaaaccttag	ccggacatgg	tggcacatgc	ctgtaatccc	agctactcag	360
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<210> 25

<211> 601

<212> DNA

<213> Homo sapien

<400> 25

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gatcccagca	ctttgggtca	aggcagtagg	attgcttgag	cccaggagtt	tgagaccagt	180
ctgggcaaca	tgtctagatc	tcctctctac	acaaattaaa	aatagctggc	atggtggcat	240
gcgcctgtag	tcctagctac	tcagaaggct	gaggtgggag	gatcatttga	gcctaggagg	300
wcaaagctgc	aatgaattat	gatttgtgcca	ctgcactcca	gccagggtga	tggagtaaga	360
ccttgtctca	aaaataaaaat	aaagtagcac	aacctcccca	agttattttt	ttccctcact	420
acaacctccc	ttcccaggac	agcttagtta	agtttgcatg	atgctttact	tctgcagatg	480
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g						601

<210> 26

<211> 601

<212> DNA

<213> Homo sapien

<220>

<221> variation

<222> (301)...(301)

